Gag_AF110965_BW_mod

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCC
TGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC
CGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAACACCG
TGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCCGAC
AAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACC
AGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAG
CCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAAC
ACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCA
ACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCCATCGCCCCCGG
CCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCACCAGCACCCTGCAGGAGCAG
ATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCA
TCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA
GGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAG
CAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACC
CCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGC
CAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCC
GCCCCGAGCCCACCGCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCA
GAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGAC
CCCCTGAGCCAGTAA

FIG. 1

Gag_AF110967_BW_mod

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCC
TGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG
AAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG
TGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCCGAC
GGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGG
CCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCC
CGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACG
ATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACG
AGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGCCCCGTGGCCCCCGGCCA
GATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCACCAGCACCCTGCAGGAGCAGATC
GCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCC
TGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGG
CCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAG
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCG
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCACCCTGGAGGAGATGATGACCGC
CTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAG
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAACC
GCAGCGAGCCCGCCGCCCCCACCGTGCCCACCGCCCCCCCCGCCGAGAGCTTCCGCTTCGA
GGAGACCACCCCCGCCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG
ACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCCCTGAGCCAGTAA

FIG. 2

Env_AF110968_C_BW_opt

--> signal peptide (1-81)
ATGCGCGTGATGGGCATCCTGAAGAACTACCAGCAGTGGTGGATGTGGGGCATCCTGGGCTTCTGGATGCTGATCA
\/--> gp120/140/160 (82)
TCAGCAGCGTGGTGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCT
GTTCTGCACCAGCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACC
GACCCCAACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACC
AGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGAC
CCTGAAGTGCCGCAACGTGAACGCCACCAACAACATCAACAGCATGATCGACAACAGCAACAAGGGCGAGATGAAG
AACTGCAGCTTCAACGTGACCACCGAGCTGCGCGACCGCAAGCAGGAGGTGCACGCCCTGTTCTACCGCCTGGACG
TGGTGCCCCTGCAGGGCAACAACAGCAACGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCTG
CCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGCACCCCCGCCGGCTACGCCATCCTGAAGTGCAACAAC
CAGACCTTCAACGGCACCGGCCCCTGCAACAACGTGAGCAGCGTGCAGTGCGCCCACGGCATCAAGCCCGTGGTGA
GCACCCAGCTGCTGCTGAACGGCAGCCTGGCCAAGGGCGAGATCATCATCCGCAGCGAGAACCTGGCCAACAACGC
CAAGATCATCATCGTGCAGCTGAACAAGCCCGTGAAGATCGTGTGCGTGCGCCCCAACAACAACACCCGCAAGAGC
GTGCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGGCGAGATCATCGGCGACATCCGCCAGGCCTACTGCATCA
TCAACAAGACCGAGTGGAACAGCACCCTGCAGGGCGTGAGCAAGAAGCTGGAGGAGCACTTCAGCAAGAAGGCCAT
CAAGTTCGAGCCCAGCAGCGGCGGCGACCTGGAGATCACCACCCACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC
TGCGACACCAGCCAGCTGTTCAACAGCACCTACAGCCCCAGCTTCAACGGCACCGAGAACAAGCTGAACGGCACCA
TCACCATCACCTGCCGCATCAAGCAGATCATCAACATGTGGCAGAAGGTGGGCCGCGCCATGTACGCCCCCCCCAT
CGCCGGCAACCTGACCTGCGAGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGACCGGCCCCAAC
GACACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCGCAACGAGCTGTACAAGTACAAGGTGG
gp120(1512)<--\/-->(1513)gp41
TGGAGATCAAGCCCCTGGGCGTGGCCCCCACCGAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGG
CATCGGCGCCGTGTTCCTGGGCTTCCTGGGCGCCGCCGGCAGCACCATGGGCGCCGCCAGCATCACCCTGACCGTG
CAGGCCCGCCTGCTGCTGAGCGGCATCGTGCAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACC
TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGACCCGCATCCTGGCCGTGGAGCGCTACCTGAAGGACCA
GCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGC
AACCGCAGCCACGACGAGATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACTACACCGACA
CCATCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGCCCTGGACAGCTG
gp140(2025)<--\/
GCAGAACCTGTGGAACTGGTTCAGCATCACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGC
CTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGCCCT
TCCAGACCCTGACCCCCAACCCCCGCGAGCCCGACCGCCTGGGCCGCATCGAGGAGGAGGGCGGCGAGCAGGACCG
CGGCCGCAGCATCCGCCTGGTGAGCGGCTTCCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGC
TACCACCGCCTGCGCGACTTCATCCTGATCGCCGCCCGCGTGCTGGAGCTGCTGGGCCAGCGCGGCTGGGAGGCCC
TGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCCTGGAGCTGAAGAAGAGCGCCATCAGCCTGCTGGACACCAT
CGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGTTCATCCAGCGCATCTGCCGCGCCATCCGCAACATC
gp160, gp41(2547)<--\
CCCCGCCGCATCCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

FIG. 3

Env_AF110975_C_BW_opt

--> signal peptide (1-72) \/-->
ATGCGCGTGCGCGGCATCCTGCGCAGCTGGCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATCTGCAGCG
gp120/140/160 (72)
GCCTGGGCAACCTGTGGGTGACCGTGTACGACGGCGTGCCCGTGTGGCGCGAGGCCAGCACCACCCTGTTCTGCGC

CAGCGACGCCAAGGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCAAC

CCCCAGGAGATCGAGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACG

AGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCCGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAAGTG

CACCAACTACAGCACCAACTACAGCAACACCATGAACGCCACCAGCTACAACAACAACACCACCGAGGAGATCAAG

AACTGCACCTTCAACATGACCACCGAGCTGCGCGACAAGAAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA

TCGTGCCCCTGAACAGCAACAGCAGCGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCTGCCC

CAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTACGCCATCCTGAAGTGCAAGAACAAC

ACCAGCAACGGCACCGGCCCCTGCCAGAACGTGAGCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGAGCA

CCCCCCTGCTGCTGAACGGCAGCCTGGCCGAGGGCGGCGAGATCATCATCCGCAGCAAGAACCTGAGCAACAACGC

CTACACCATCATCGTGCACCTGAACGACAGCGTGGAGATCGTGTGCACCCGCCCCAACAACAACACCCGCAAGGGC

ATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGAGAACATCATCGGCGACATCCGCCAGGCCCACTGCAACA

TCAGCGCCGGCGAGTGGAACAAGGCCGTGCAGCGCGTGAGCGCCAAGCTGCGCGAGCACTTCCCCAACAAGACCAT

CGAGTTCCAGCCCAGCAGCGGCGGCGACCTGGAGATCACCACCCACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC

TGCAACACCAGCAAGCTGTTCAACAGCAGCTACAACGGCACCAGCTACCGCGGCACCGAGAGCAACAGCAGCATCA

TCACCCTGCCCTGCCGCATCAAGCAGATCATCGACATGTGGCAGAAGGTGGGCCGCGCCATCTACGCCCCCCCCAT

CGAGGGCAACATCACCTGCAGCAGCAGCATCACCGGCCTGCTGCTGGCCCGCGACGGCGGCCTGGACAACATCACC

ACCGAGATCTTCCGCCCCCAGGGCGGCGACATGAAGGACAACTGGCGCAACGAGCTGTACAAGTACAAGGTGGTGG
gp120(1509)<--\/-->(1510)gp41
AGATCAAGCCCCTGGGCGTGGCCCCCACCGAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGGCAT

CGGCGCCGTGATCTTCGGCTTCCTGGGCGCCGCCGGCAGCAACATGGGCGCCGCCAGCATCACCCTGACCGCCCAG

GCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACATGC

TGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCATCGAGCGCTACCTGAAGGACCAGCA

GCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAAC

AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGGACAAGGAGATCAGCAACTACACCGGCATCA

TCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCCGCAA
gp140(2022)<--\/
CAACCTGTGGAGCTGGTTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCTG

ATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCC

AGACCCTGACCCCCAACCCCCGCGGCCTGGACCGCCTGGGCCGCATCGAGGAGGAGGGCGGCGAGCAGGACCGCGA

CCGCAGCATCCGCCTGGTGCAGGGCTTCCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCCTGTTCAGCTAC

CACCGCCTGCGCGACCTGATCCTGGTGACCGCCCGCGTGGTGGAGCTGCTGGGCCGCAGCAGCCCCCGCGGCCTGC

AGCGCGGCTGGGAGGCCCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCCTGGAGCTGAAGAAGAGCGCCAC
gp160, gp41(2565)<--\
CAGCCTGCTGGACAGCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGATCCAGCGCATCTAC

CGCGCCTTCTGCAACATCCCCCGCCGCGTGCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

FIG. 4

Gag_AF110965_BW_opt

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCCTGCGCCCCGG

CGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGAAGTTCGCCCTGAACC

CCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCCGCCCTGCAGACCGGC

AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTGCG
C

CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGATCCAGCAGGCCG

AGGCCGCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC

CAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGT

GATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGG
G T

GCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTG

CACCCCGTGCACGCCGGCCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC

CACCAGCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGCGACATCTACA

AGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCAAG
G G

CAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCAC

CCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCC

TGCGCGCCCTGGGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGC
T G

CACAAGGCCCGCGTGCTGGCCGAGGCCATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTT
G

CAAGGGCCCCCGCCGCATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCG
G C

CCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG

GCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCGA

GCCCACCGCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGCAAGG

ACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA

FIG. 5

Gag_AF110967_BW_opt

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCCGG

CGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGGGCTTCGCCCTGAACC

CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGC

ACCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTGCG
C

CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGACCCAGCAGGCCA
TC

AGGAGGCCGACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAG

GCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGAT

CCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGGGCG
G T

GCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCAC

CCCGTGCAGGCCGGCCCCGTGGCCCCCGGCCAGATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCAC

CAGCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTACAAGC

GCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAG
G G

GGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGGCCACCCA

GGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGC

GCGCCCTGGGCCCCCGGCGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAC
T C

AAGGCCCGCGTGCTGGCCGAGGCCATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTT
G

CAAGGGCCCCCGCCGCAACGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCG
G C

CCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG

GCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAACCGCAGCGA

GCCCGCCGCCCCCACCGTGCCCACCGCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCC

CCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGC

GGCCCCCTGAGCCAGTAA

FIG. 6